

Domain organization of MTSP3

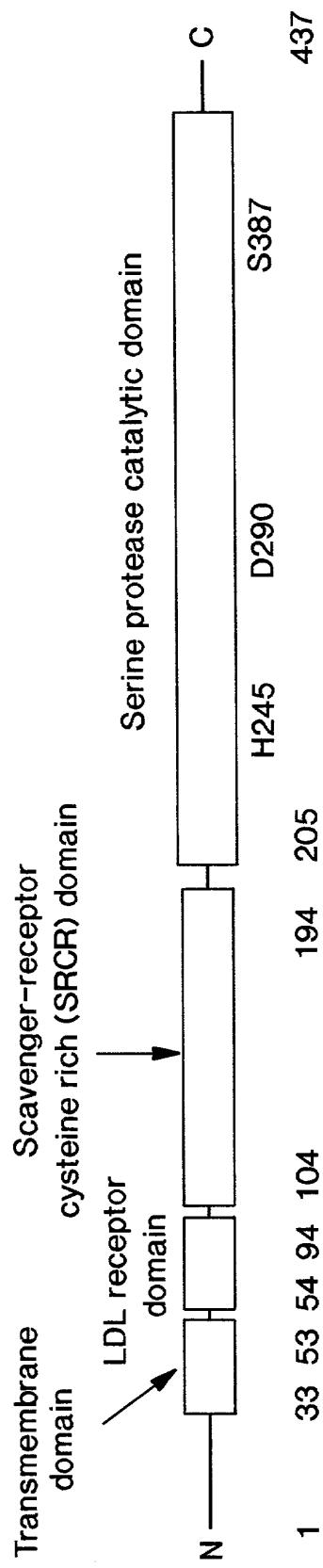


FIG. 1

Splice variant and domain organization of MTSP4

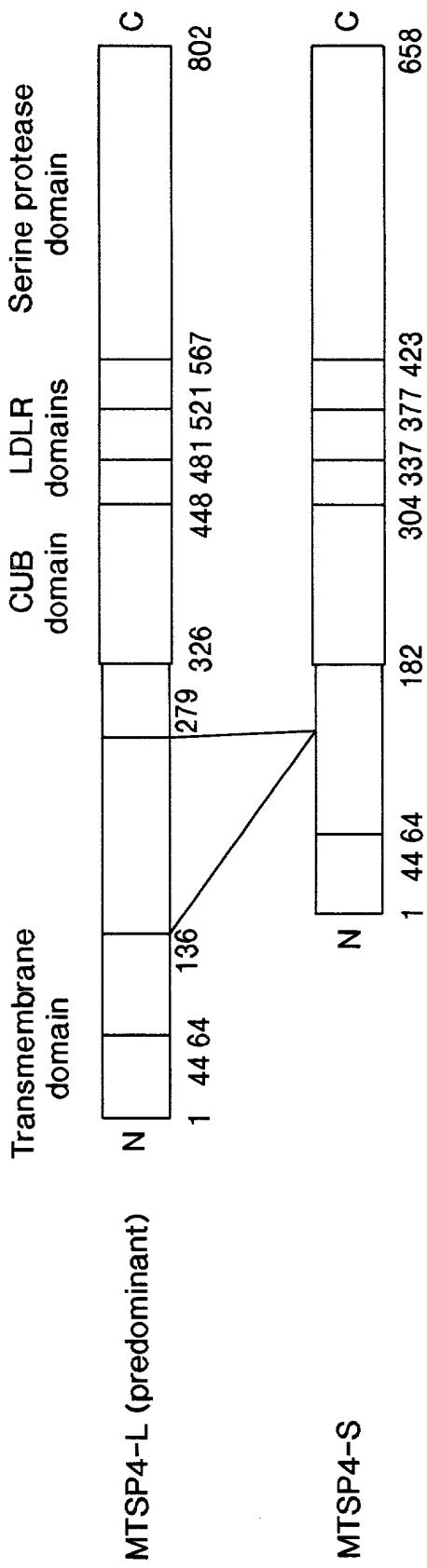


FIG. 2

Domain organization of human MTSP6

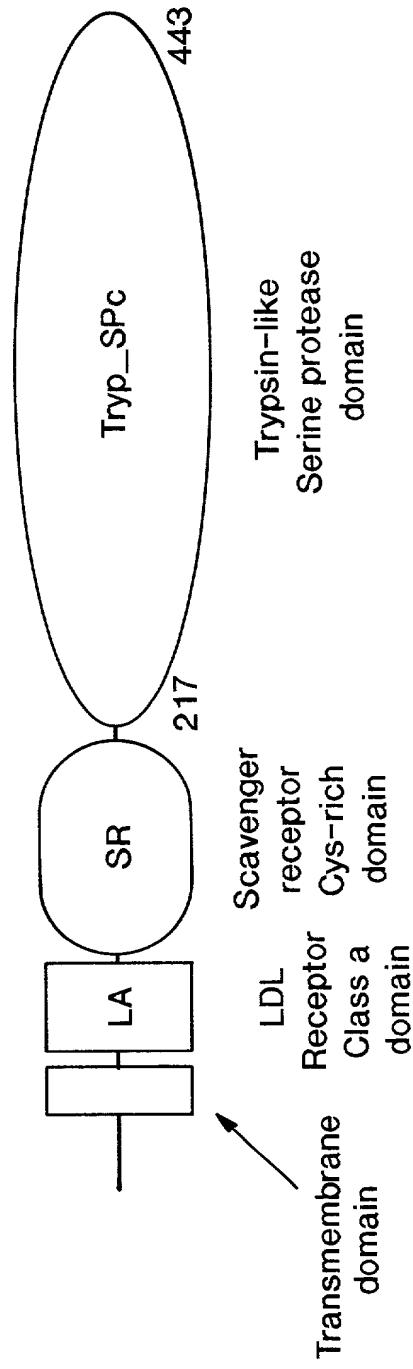


FIG. 3

MTSP3 194 LACGKS-----LKTPRVVGEEASVDSWPWQVSIQYDKQHVCAGGSILD 236
205
MTSP4-S 396 PQCDGRPDCRDGSDEEHCECGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIA 455
424
MTSP4-L 540 PQCDGRPDCRDGSDEEHCECGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIA 599
568
MTSP6 205 TACGHR-----RGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCAGGSVIT 248
217 +

MTSP3 237 PHWVLTAACFRKHTDVFN--WKVRAGSDKLGS---FPLSLAVAKIIIEFNPMYPKDND 290

MTSP4-S 456 DRWVITAAHCFQEDSMASTVLTWFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYD 515

MTSP4-L 600 DRWVITAAHCFQEDSMASTVLTWFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYD 718

MTSP6 249 PLWIITAAHCVYDLYLPKS--WTIQVGLVSLD--NPAPSHLVEKIVYHSKYKPKRLGND 304

MTSP3 291 IALMKLQFPLTFSGTVRPICLFFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQV 350
*
MTSP4-S 516 VALLQLDHPVVRSAAVRPVCLPARSHFFEPGLHCWITGWGALRE-GGPISNALQKVDVQL 574
*
MTSP4-L 660 VALLQLDHPVVRSAAVRPVCLPARSHFFEPGLHCWITGWGALRE-GGPISNALQKVDVQL 718
*
MTSP6 305 IALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATED-GGDASPVLNHAAPVPL 363
*
MTSP3 351 IDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTQCQGDSSGPLMYQSDQ--WHVVGIVSWG 408

MTSP4-S 575 IPQDLCS--EVYRYQVTPRMLCAGYRKKGKDACQGDSSGPLVCKALSGRWFLAGLVSWGL 632

MTSP4-L 719 IPQDLCS--EVYRYQVTPRMLCAGYRKKGKDACQGDSSGPLVCKALSGRWFLAGLVSWGL 776

MTSP6 364 ISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSSGPLVCQERR-LWKVLVGATSGI 442

MTSP3 409 GCGGPSTPGVYTKVSAYLNWIYNVWKAEL 437

MTSP4-S 633 GCGRPNYFGVYTRITGVISWIQQVVT 658

MTSP4-L 777 GCGRPNYFGVYTRITGVISWIQQVVT 802

MTSP6 423 GCAEVNPKPGVYTRVTSFLDIHEQMERDLKT 453

▽ cleavage site

+ potential glycosylation site

* unpaired cysteine

FIG. 4